Structures from crystals with large unit cells

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The orbiviruses belong to *Reoviridae* and are mammalian viruses with insect vectors. The rotaviruses and reoviruses, which cause significant human disease, belong to the same family. Bluetongue virus is the classic orbivirus; it has a 700 Å diameter core, which is robust and penetrates the host cell intact; it then operates as a factory, extruding mRNA, which is translated to form more virus particles. The core contains proteins with enzymatic activity and much larger numbers of proteins VP3 and VP7. VP7 forms the outer surface of the core and is present at the level of 780 copies per core, arranged on a T=13 lattice. We have combined information from the x-ray structures of VP73 with that from electron cryo-microscopy (Prasad, unpublished) to get a rough picture of this structure, which, at about 100 million Daltons, is larger than any virus structure previously analyzed by crystallography.

To establish the atomic structure of the core we have perfomed a crystallographic analysis. We have separately crystallized the whole core of 2 serotypes: BTV-1 and BTV-10. BTV-1 crystallizes in space group P2₁2₁2, a=798Å, b=825Å, c=756Å (ref 4), BTV-10 crystallizes in space group P4₁2₁2, a=b=1120Å, c=1592Å. Data have been collected at the SRS (UK) & ESRF (France) for BTV-1 and at the ESRF for BTV-10. Both structures have been solved using the cry-em phasing model. The talk will outline some of the problems in the crystallographic analysis and give a flavor of the results that have emerged.

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